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Minimum
Maximum
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No.
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 Score
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seq length:
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2046
1 ELVMTQSPSSLTVT
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Issued_patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/Backfiles1.pep:*
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  Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                    Length
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    BB
             US-09-948-004-18
US-08-263-911-9
US-08-263-911-9
US-08-166-750-19
US-09-166-093-19
US-09-166-093-19
US-09-166-094-19
US-09-166-094-19
US-09-166-094-19
US-09-443-213-19
US-09-456-086-2
US-09-956-086-2
US-09-9791-578-4
US-09-9791-578-4
US-09-9791-540-6
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US-08-353-445-4
US-08-353-445-4
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Biocceleration
Sequence 18, Appl
Sequence 9, Appli
Sequence 19, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 4, Appli
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43.5	43.5	43.5	43.5	43.5	43.5	43.5	43.7	43.7	45.2	45.2	45.2	45.3	45.3	45.4	45.4	45.4	45.4
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US-07-935-695-12	US-08-463-903-15	US-08-463-903-12	935	US-08-463-903-10	US-07-935-695-17	US-08-463-903-17	US-07-935-695-8		PCT-US95-12840-8	US-08-515-903A-8	US-08-323-445A-8	US-09-791-578-2	US-09-791-540-2	US-09-102-716-16	US-09-364-088-16	US-09-188-082-16	US-08-661-052-16
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ALIGNMENTS

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Sequence 18, Application US/09948004

Patent NO. 672358

GENERAL INFORMATION:

APPLICANT: MACK, Matthias

TITLE OF INVENTION: Antibody and/or chemokine cointile of INVENTION: immunological disorders

FILE REFERENCE: E 2411 EP

CURRENT APPLICATION NUMBER: US/09/948,004

CURRENT FILING DATE: 2001-09-05

NUMBER OF SEG ID NOS: 34

SOFTWARE: PatentIn Ver. 2.1

SEG ID NO 18
                                                                                                                                  US-09-948-004-18
                                                                                                                                                                                                                                                                                                                                                                                                    US-09-948-004-18
                                                      Query Match
Best Local Similarity
Matches 278; Conserv
                                                                                                                                               LENGTH: 495
TYPE: PRT
ORGANISM: Mus sp.
                 1 ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR ::|:|||||||| |: |:||:||:||:||
72.6%; ilarity 74.7%; Conservative 34
                                                                    34;
                                                                 Score 1484.5; | Pred. No. 2.4e-: 34; Mismatches
                                                                    2.4e-102;
ches 53;
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                                                                    Indels
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                                                                    Gaps
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174 HPSDSETRLNOKFNDRATLTVDKYSSTAYIOLSSPTSEDSAVYYCARGEYYYGIFDYWGO

FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRUWDEPMDYWGQ

ĠĠŚĠĠĠĠŚQVQ-ĹQQPĠĀGRVRPĠĀŚVKĽŚĊKĀŚGYSFTSYWMNWVKQRPGQGLEWIGMI

GGSGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDI 180

GTTVTVSSGGGGSDIKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEW

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YWGQGTTLTVSS 372

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US-08-263-911-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/263,911
FILING DATE: 21-JUN-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/990,263
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ulmer, Duane C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-41,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Mezes, Peter S
APPLICANT: GOUTLLE, Brian B
TITLE OF INVENTION: MULTIVALENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. U
STREET: P.O. Box 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (517) 636-8104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P.O. CITY: Midland
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                        271
                                                                                                     231
                                                                                                                                            202
                                                                                                                                                                   171 GHGLEWIGDIFPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRN 230
                                                           262 ----MAYWGQGTSVTVSSLSADDAKKDAAKKDDAKKDDAKKDLEVQLQQSDAELVKPGAS
                                                                                                                                                                                                                       143 KDAAKKDDAKKDLEVQ-LQQSDAELVKPGASVKISCKASGYTFTDHAIHWVKQNP 201
                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                          61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG 120
                                                                                                                                                                                                                                                                                                                                                                                    23 DIVMSQSPSSLPVSVGEKVTLSCKSSQSLLYSGNQKNYLAWYQQKPGQSPKLLIYWASAR
                                                                                                                                                                                                                                                                                                                                                                                                                         1 BLVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR 60
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VKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYNQKFKDKATLTTDKSSS 330
                                                                                                                                          EQGLEWIGYFSPGNDDFKYNERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLN
                                                                                                                                                                                                                                                    GGSGGGGS-----EVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRP 170
                                                                                                     WDEPMDYWGQGTTVTVSSGGGGS----
                                                                                                                                                                                                                                                                                                   ESGVPDRFTGSGSGTDFTLSISSVKTEDLAVYYCQQYYSYPLTFGAGTKLVLKLSADDAK 142
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23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.9%; Score 1287.5; DB
64.2%; Pred. No. 1.1e-87;
tive 37; Mismatches 68
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Patent No. 5
                                                                                                                                                                                                                                                                       Matches 265;
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/796

PILING DATE: 25-NOV-1991

ATTORNEY AGENT INFORMATION:

NAME: Goldstein, Jorge A.

REGISTRATION NUMBER: 29,021
                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/392,338A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Filpula, David
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 22-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 TAYMQLSSLTSEDSAVYYCARYYDDHYCLDYWGQGTTLTVSS 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 VKISCKASGYTFTDHAIHWVKQNPEQGLEWIGYFSPGNDDFKYNERFKGKATLTADKSSS 377
181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDBPMDYWGQ 240
                                                                                                                                      61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLIFGAGTKLEIKGGGGSGG 120
                                                                                                                                                                                                                      1 ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20005
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5869620
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                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                ESGVPDRFTGSGSGTDFTLSISSVKTEDLAVYYCQQYYSYPLTFGAGTKLVLK-GST8GS 119
                                                                                                                                                                                          DVVMSQSPSSLPVSVGEKVTLSCKSSQSLLYSGNQKNYLAWYQQKPGQSPKLLIYWASAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAYVQLNSLTSEDSAVYFCTRSLN----MAYWGQGTSVTVSS 415
                                    GKSSEGKGQVQ-LQQSDAELVKPGASVKISCKASGYTFTDHAIHWVKQNPEQGLEWIGYF 178
                                                                        GGSGGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D.C
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1100 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood, James F
Hardman, Karl
                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whitlow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (202)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371-2600
                                                                                                                                                                                                                                                                                       62.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 07/796,936
                                                                                                                                                                                                                                                                  ; Score 1283; DB 1; ; Pred. No. 2.1e-87; 37; Mismatches 59;
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e, NW
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                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                           Length 483;
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                                                                                                                                                                                                                                                                         Gaps
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Gaps

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60

178

248

234

298

414

354 254 294

470

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RESULT 4
US-09-166-750-19
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                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/392,338
APPLICATION UNMBER: US 07/989,846
FILING DATE: 22-FEB-1995
PRIOR APPLICATION UNMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION UNMBER: US 07/796,936
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Whitle
          TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/166,750
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Filpula, David
APPLICANT: Rollence, Michelle
TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                           NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255
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 483 amino acids
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Bird, Robert
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-166-750-19
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US-09-166-093-19
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Best Local Similarity
Matches 265; Conserv
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,093
                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                          APPLICANT: Hird, Robert
APPLICANT: Filpula, David
APPLICANT: Filpula, David
APPLICANT: Rollence, Michelle
APPLICANT: Rollence, Michelle
TITLE OF INVENTION: Multivalent Antigen-Binding
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                   STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                     ZIP: 20005
                                                                                                                                    COUNTRY:
                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EWIGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYC 358
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                                                                                                                                                                                       3E: Sterne, Kessler, Gold
1100 New York Avenue, NW
                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                            Wood, James F
Hardman, Karl
                                                                                                                                                                                                                                                                                                                                                            Whitlow, Marc
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53.8%;
                                                                                                                                                                                                        Kessler, Goldstein & Fox P.L.L.C.
                                   Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  483
     us/09/166,093
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Pred. No. 2.1e-87;
                                      #1.25
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RESULT 6
US-09-172-019-19
j Sequence 19, Application US/09172019
j Patent No. 6103889
j GENERAL INFORMATION:

// MOLECULE TYPE: protein
US-09-166-093-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: COLUMN TO THE PROPERTY OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
TYPE: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: Herewit CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000B
TELECOMMUNICATION INFORMATION:
APPLICANT: Whitlow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 22-FF
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                                                                                                                                                                                                                                           MAYWGQGTSVTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGSGGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYMLGWVKQRPGHGLEWIGDI 180
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ilarity 53.8%;
Conservative 3
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; Pred. No. 2.1e-87;
37; Mismatches 59;
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INFORMATION FOR SEQ ID NO:
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FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Bird, Robert
APPLICANT: Filpula, David
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain
TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
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REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.
TELECOMMUNICATION INFORMATION:
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TOPOLOGY: linear
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LIYWASARESGVPDRFTGSGSGTDFTLSISSVKTEDLAVYYCQQYYSYPLTFGAGTKLVL 354
                                                                                                                                                                                                                                              SPGNDDFKYNERFKGKÄTLTÄDKSSSTAYVQLNSLTSEDSAVYFCTRSLN----MAYWGQ 234
                                                                                                                                                                                                                                                                              FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDBPMDYWGQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESGYPDRFTGSGSGTDFTLSISSYKTEDLAVYYCQQYYSYPLTFGAGTKLVLK-GSTSGS
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US-09-166-094-19
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                                                                                                    ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-166-094-19
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                                        Query Match
Best Local Similarity
Matches 265; Conserv
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                               NAME: GOLDStein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/796,936 FILING DATE: 25-NOV-1991 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 1
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Filpula, David
APPLICANT: Rollence, Michelle
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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KGSTSGSGKSSEGKGQVQLQQSDAELVKPGASVKISCKASGYTFTDHAIHWVKQNPEQGL
ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR
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Wood, James F.
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Bird, Robert
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                                             62.7%; Score 1283; DB 2; 53.8%; Pred. No. 2.1e-87; tive 37; Mismatches 59;
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                                                                       Length 483;
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US-09-443-213-19
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181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GGSGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDI 180
                                                                                                                                                                                                                                                                                                                                             295 LIYWASARESGVPDRFTGSGSGTDFTLSISSVKTEDLAVYYCQQYYSYPLTFGAGTKLVL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGSGG 120
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                                                                                                                                                                                                                          KGSTSGSGKSSEGKGQVQLQQSDAELVKÞGASVKISCKASGYTFTDHAIHWVKQNÞEQGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPGNDDFKYNERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLN----MAYWGQ 234
MAYWGQGTSVTVS 483
                                                                                                             EWIGYFSPGNDDFKYNERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTSVTVSSDVVMSQSPSSLPVSVGEKVTLSCKSSQSLLYSGNQKNYLAWYQQKPGQSPKL 294
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                                                                                                                                                                                                                                                                                      ----IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGL 298
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Sequence 19, Application US/09443213 Patent No. 6515110 MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/443, 213
FILING DATE: Herewith
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/166,094
FILING DATE: 05-OCT-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992 APPLICANT: Whitlo:
APPLICANT: Wood, COMPUTER READABLE FORM: MEDIUM TYPE: Floppy APPLICANT: Filpula, David
APPLICANT: Rollence, Michelle
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS: CITY: Washington E: Sterne, Kessier, Go 1100 New York Avenue, Bird, Robert Hardman, Karl Wood, James Whitlow, Marc U.S.A. Kessler, Goldstein & Fox P.L.L.C. ork Avenue, NW Version #1.25

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RESULT 9
US-08-263-911-7
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                                                                                                                                                        Sequence 7, Application US/08263911
Patent No. 5877291
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.7%; Score 1283; DB 2; Best Local Similarity 53.8%; Pred. No. 2.1e-87;
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APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                               APPLICANT: Mezes, Peter S
APPLICANT: GOURTIC, Brian B
TITLE OF INVENTION: MULTIVALENT S:
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
TOPOLOGY: linear
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STREET: P.O. B
CITY: Midland
STATE: MI
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                                                                                                                                                                                                                                                                                       MAYWGQGTSVTVS
                                                                                                                                                                                                                                                                                                                                                                               EWIGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTVTVSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPGNDDFKYNERFKGKATLTADKSSSTÄYVQLNSLTSEDSAVYFCTRSLN----MAYWGQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKSSEGKGQVQ-LQQSDAELVKPGASVKISCKASGYTFTDHAIHMVKQNPEQGLEWIGYF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGSGGGS8VQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESGVPDRFTGSGSGTDFTLSISSVKTEDLAVYYCQQYYSYPLTFGAGTKLVLK-GSTSGS
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                                                                                                                                                                                                                                                                                                                                                          EWIGYFSPGNDDFKYNERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIYWASARESGVPDRFTGSGSGTDFTLSISSVKTEDLAVYYCQQYYSYPLTFGAGTKLVL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTSVTVSSDVVMSQSPSSLPVSVGEKVTLSCKSSQSLLYSGNQKNYLAWYQQKPGQSPKL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                   KGSTSGSGKSSEGKGQVQLQQSDAELVKPGASVKISCKASGYTFTDHAIHWVKQNPEQGL
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                                                                                                                                                                                                                                                                                         483
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                                                                                                          SINGLE CHAIN ANTIBODIES
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RESULT 10

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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-263-911-7
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FILING DATE: 21-JUN-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,263
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ulmer, Duane C
REGISTRATION NUMBER: C-41,014
REFERENCE/DOCKET NUMBER: C-41,014
REFERENCE/DOCKET NUMBER: G-41,014
TELECOMMUNICATION: 1NFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 261;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 4864111967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
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LENGTH: 553 amino acid
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ZIP: 486
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STRANDEDNESS: sir
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                                                                     438
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498
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                                                                                                                                                                                                                                                                                                                                                                                                                                     KDAAKKDDAKKDDAKKDLEVQ-LQQSDAELVKPGASVKISCKASGYTFTDHAIHWVKQNP
                      YNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLDYMGQGTTLTVSS 372
                                                                                                       --IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTN 312
                                                                                                                                                                                                                KVTLSCKSSQSLLYSGNQXNYLAWYQQKPGQSPKLLIYWASARESGVPDRFTGSGSGTDF 377
                                                                                                                                                                                                                                                                                                                             WDEPMDYWGQGTTVTVSS------
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                                                                     LEVQLQQSDAELVKPGASVKISCKASGYTFTDHAIHWVKQNPEQGLEWIGYFSPGNDDFK 497
                                                                                                                                             TLSISSVKTEDLAVYYCQQYYSYPLTFGAGTKLVLKLSADDAKKDAAKKDDAKKDDAKKD
                                                                                                                                                                                                                                                                                          ----MAYWGQGTSVTVSSLSADDAKKDAAKKDDAKKDDAKKDLDIVMSQSPSSLPVSVGB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESGVPDRFTGSGSGTDFTLSISSVKTEDLAVYYCQQYYSYPLTFGAGTKLVLKLSADDAK 142
YNERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLN----MAYWGQGTSVTVSS
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Pred. No. 1.9e-83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 553;
                                                                                                                                                                                                                                                          Gaps
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82 60

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317

254

254

261

248

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; OTHER INFORMATION: Description of Artificial Sequence: ompA-FLAG-scFv (anti-
; OTHER INFORMATION: HAG)-gene IIIss encoded by phage vector fhaglA (circular)
US-09-495-880A-11
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                                                                                                                                                                                                                                                                                                                                                    RESULT 11
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PRIOR PILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: EP 97 11 3319.4
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09495880A Patent No. 6667150
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Best Local Similarity
                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09069821 Patent No. 6323322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL METHOD AND PHAGE FOR THE IDENTIFICATION OF TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIC TITLE OF INVENTION: (POLY) PEPTIDE COMPLEX FILE REFERENCE: MORPHO/9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: RUDERT, FRITZ
APPLICANT: GE, LIMING
APPLICANT: ILAG, VIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/495,880A CURRENT FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 456
                                                                                                                     APPLICANT: SHORR, ROBERT
APPLICANT: WHITLOW, MARC
APPLICANT: LEE, LIHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION J.
NUMBER OF SEQUENCES: 33
                                                                                                      CORRESPONDENCE ADDRESS:
                                                ADDRESSEE: STERNE, KESSLER, STREET: 1100 NEW YORK AVE., CITY: WASHINGTON
                                STATE: DC
               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164
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                 USA
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                                                                     GOLDSTEIN & FOX P.L.L.C
NW, SUITE 600
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RESULT 12
US-09-956-086-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acids
TYPE: lenino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 74.0%;
Matches 185; Conservative 2:
                                                                                                               Sequence 2, Application US/09956086
Patent No. 6743896
GENERAL INFORMATION:
APPLICANT: FILPULA, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/067,341
APPLICATION DATA:
PILLING DATE: 02-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/063,074
FILLING DATE: 27-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050,472
FILLING DATE: 23-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/044,449
FILLING DATE: 30-APR-1997
APPLICATION NUMBER: US 60/044,449
FILLING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.228000
TELECOMMUNICATION INFORMATION:
THELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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LEE, LIHSYNG S.
INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION
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                                                                              WANG, MAOLIANG
SHORR, ROBERT
                                                              WHITLOW, MARC
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                  AND USES THEREOF
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RESULT 13
US-09-956-087-2
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                   Sequence 2, Application US/09956087 Patent No. 6743908 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 185;
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APPLICATION UNMBER: 09/069,821

PILING DATE: <UNKNOWN:

APPLICATION NUMBER: US 60/063,074

FILING DATE: 27-OCT-1997

APPLICATION NUMBER: US 60/050,472

FILING DATE: 23-UN-1997

APPLICATION NUMBER: US 60/044,449

FILING DATE: 30-APR-1997

APPLICATION NUMBER: US 60/044,449

FILING DATE: 30-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0977.228000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)371-2600

TELEPHONE: (202)371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,086
FILING DATE: 20-Sep-2001
CINSCREIGNATON. (Theory)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: STERME, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
APPLICANT: FILPULA, DAVID
                                                                                                                                                                                                                                                                             181 YFSPGNDDFKYNERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLN----
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                                                                                                                                                                                     GQGTSVTVSN
                                                                                                                                                                                                                                                                                                                             DIFPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDBPMDYW 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESGVPDRFTGSGSGTDFTLSISSVKTEDLAVYYCQQYYSYPLTFGAGTKLVLKGSTSGSG 120
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TOPOLOGY: Innear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-956-087-2
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 09/069,821

FILING DATE: 1998-04-30

APPLICATION NUMBER: US 60/063,074

FILING DATE: 27-CCT-1997

APPLICATION NUMBER: US 60/050,472

FILING DATE: 23-UUN-1997

APPLICATION NUMBER: US 60/044,449

FILING DATE: 30-APR-1997

APPLICATION NUMBER: US 60/044,449

FILING DATE: 30-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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SHORR, ROBERT
WHITLOW, MARC
LEE, LIHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                                                                                  DIFPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYW 238
                                                                                                                                                                        GGGSGGGGSEVQL-LEQSGAELVRPGTSVKISCKASGYAFTNYMLGWVKQRPGHGLEWIG 178
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                                    GOGTTVIVSS 248
                                                                                                                                                    KPGSGEGSTKGQVQLQQSDAELVKPGASVKISCKASGYTFTDHAIHWVKQNPEQGLEWIG
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COUNTRY: USA
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GOGTSVTVSN 246
                                                                          YFSPGNDDFKYNERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLN----MAYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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TELEPAX: (202)371-2540
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RESULT 14 US-09-393-627B-28

Sequence 28, Application US/09393627B Patent No. 6455314

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CURRENT APPLICATION NUMBER: US/09/393,627B
CURRENT FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/099,851
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-12
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-420-592A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
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LENGTH: 354
TYPE: PRT
ORGANISM: Anti-HA ScFv fused in frame with 2 C-terminal myc epitopes
ORGANISM: Anti-HA ScFv fused in frame with 2 C-terminal myc epitopes
PDGF receptor transmembrane anchor (Anti-HA pseudo-receptor)
S-09-393-627B-28
                                                                                 APPLICANT: Filpula, David R.
APPLICANT: Wang, Macliang
APPLICANT: Whitlow, Marc D.
APPLICANT: Whitlow, Marc D.
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: NO. 6333396el Method for Targeted Delivery of Nucleic Acids
FILE REFERENCE: 0977.230001 1
CURRENT APPLICATION NUMBER: US/09/420,592A
CURRENT FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 257
TYPE: Nom
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09420592A Patent No. 6333396 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Kovesdi, Imre
APPLICANT: Roelvink, Petrus I
APPLICANT: Bruder, Joseph T.
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TITLE OF INVENTION: Alternatively Targeted Adenovirus
                      ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sFv
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                                                             181 YFSPGNDDFKYNERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLN----MAYW
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                                                                                                                           121 KPGSGEGSTKGQVQLQQSDAELVKPGASVKISCKASGYTFTDHAIHWVKQNPEQGLEWIG
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GOGTSVTVS 245
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pelB leader/Ig hea Ig kappa chain V r Ig heavy chain Ig kappa chain pre Ig kappa chain F v an Ig kappa chain F v an Ig kappa chain F v an Ig kappa chain Ig ka
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45	44	43	42	41	40	39	38	37	36	35	34	ω G	32	31	30
484	484	484.5	484.5	485	486	486.5	487	487.5	488	488.5	489.5	490	490.5	492	492
23.7	23.7	23.7	23.7	23.7	23.8	23.8	23.8	23.8	23.9	23.9	23.9	23.9	24.0	24.0	24.0
141	140	115	112	140	121	112	120	112	118	122	139	140	120	446	246
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A39276	PH1498	A56700	S41393	PH1488	A26405	809970	S25175	843103	S38565	S24287	MHMS18	PH1484	B22769	S40295	S38950
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ALIGNMENTS

PC4402
pc1B leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion C;Species: synthetic
C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998
C;Accession: PC4402
C;Accession: PC4402
R;Suzuki, C; Ueda, H.; Suzuki, E.; Nagamune, T.
J. Biochem. 122, 322-329, 1997 A,Title: Construction, bacterial expression, and A,Reference number: PC4402
A,Accession: PC4402 밁 Ş 밁 Ś 밁 Ś 밁 S A;Molecule type: DNA A;Residues: 1-287 <SUZ> A;Cross-references: UNIPARC:UPI000017CF08 C;Keywords: fusion protein RESULT δ Query Match Best Local Similarity Matches 138; Conserv 113 258 198 168 142 82 61 26 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEI-----LRNWDEP-MDYWGOGTTVTVSSG 249 KDDAKKDDAKKDDAKKDG---QVQ-LQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVK ----KGGGGSGGGGGGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVK 167 APGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLSSADDAK 141 YDYYGSSYFDYWGQGTTLTVSSG QRPGHGLEWIGDIFPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCAR QRPGRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMOLSSLTSEDSAVYYCAR 30.8%; milarity 52.5%; Conservative 2 25; Score 631; DB 4; Pred. No. 1.6e-33; 5; Mismatches 78 DB 4; characterization of hapten-specific 78; Length 287; Indels 22; Gaps 227 197 112 257 81 6 protein 8in

Ig kappa chain V region (anti-DNA, S57VK, S4VK, S54VK, S7VK and S204VK) - m C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000 C;Accession: PLO263 R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-J. Exp. Med. 171, 265-297, 1990 A;Tile: Anti-DNA antibodies from autoimmune mice arise by clonal expansion A;Reference number: PLO231; MUID:90111618; PMID:2104919

Marshak-Rothstein,

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and somatic

S7VK and S204VK) - mouse

(fragme

RESULT PL0263

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A; Molecule type: mRNA
A; Residues: 1-113 <SHL>
A; Residues: 1-113 <SHL>
A; Cross-references: UNIPARC: UPI0000176AF7
C; Superfamily: immunoglobulin V region; imm
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 1-23/Region: framework 1
Ig kappa chain V region (253.15D10) - m (Species: Mus musculus (house mouse) C;Date: 10-Feb-1989 #sequence_revision C;Accession: F30538 R;Clafiln, J.L.; Berry, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-220 <SCH>
A;Residues: 1-220 <SCH>
A;Crossereferences: UNIPARC:UPI0000114E12; GB:M23626; GB:J04061; NID:g533234; PIDN:AAA3:
A;Crossereferences: UNIPARC:UPI0000114E12; GB:M23626; GB:J04061; NID:g533234; PIDN:AAA3:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, U.; Biol. Chem. 263, 17100-17105, 1988
A;Title: Preliminary crystallographic data, A;Reference number: A92686; MUID:89034213;
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A31790
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F;95-103/Region: complementari
F;104-113/Region: framework 4
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                                                                                                                                                                                                                                                                                            --RADAAPTVSIFPPSSEQLTSGGASV
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; Pred. No. 2.5e-29;
19; Mismatches 48;
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Pred. No. 1.9e-30;
                                                                                           mouse (fragment)
                                             10-Feb-1989 #text_change 21-Jan-2000
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R;Claflin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody
A;Reference number: A30534; MUID:89035545; PMID:3141511
A;Accession: E30538
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C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 21-Jan-2000
C;Accession: E30538
                                                                                                                                                                                                Ig kappa chain V region (anti-DNA, D20VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0364
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C;Keywords: het
F;16-96/Domain:
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A;Cross-references: UNIPARC:UPI0000176CD4
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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E30538
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(;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
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A;Cross-references: UNIPARC:UPI0000176AFB C;Superfamily: immunoglobulin V region; in C;Keywords: heterotetramer; immunoglobulii
                                                                                                                R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pi
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise
A;Reference number: PL0231; MUID:90111618; PMID:2104919
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                                                           A; Molecule type: mRNA
A; Residues: 1-113 <SHL>
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Pred. No. 1.8e-28;
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Pred. No. 1.1e
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immunoglobulin

immunoglobulin homology

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R;Sequeira, A.; Avrameas, S.; Jouvin-Marche, E.
Immunogenetics 36, 15-21, 1992
A;Title: Molecular characterization of the variable regions of A;Reference number: $38807; MUID:92267566; PMID:1587549
A;Accession: $38807
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <SEQ>
A;Cross-references: UNIPARC:UPI0000176CA6; EMBL:X59816
A;Cross-references: UNIPARC:UPI0000176CA6; EMBL:X59816
A;Note: the authors translated the codon GGC for residue 1 as A C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;1-23/Region: framework 1
F;16-96/Domain: immunoglobulin homology <IMM
F;24-40/Region: complementarity-determining
F:41-55/Region: framework 2
F-41-55/Region: framework 2
                                                                                                                                                                                                                                                                                                                  RESULT 8
S38807
                                                                                                                                                                                                                               Ig light chain V-J region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1994 #sequence_revision 26-May-1995
C;Accession: S38807
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A;Status: preliminary
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J. Immunol. 138, 3060-3068, 1987
A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced A;Reference number: A30556; MUID:87196439; PMID:3106498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain V region (6D10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Feb_1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000
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nilarity 91.2%;
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Pred. No. 4.4e-28;
6; Mismatches 4
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Pred. No. 1.2e-27;
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A;Experimental source: strain BALB/c
C;Comment: This chain is obtained from an IgG2a monoclonal antibody
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-139/Domain: Ig heavy chain V region #status predicted <IGV>
F;34-117/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
C;Accession: PS0024
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G30535
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A;Title: Cloning and characterization of cDNAs coding for the heavy and light chains A;Reference number: PS0023; MUID:89232725; PMID:3149944
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J. Immunol. 138, 3060-3068, 1987
A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced A;Reference number: A30556; MUID:87196439; PMID:3106498
A;Accession: G30535
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V region (266) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 23-Feb-1989 #sequence_revision 23-Feb-19 C;Accession: G30535
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A; Residues: 1-139 < MAR>
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A;Cross-references: UNIPARC:UPI0000176AF6
A;Note: the sequence was determined from the differentiated
C;Superfamily: immunoglobulin V region; immunoglobulin homol
C;Keywords: heterotetramer; immunoglobulin
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A; Residues: 1-107 < CLA>
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Pred. No. 1.5e-27;
5; Mismatches 6
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Pred. No. 1.9
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Ig kappa chain V region (5G4) - mouse (fragment)
(;Species: Mus musculus (house mouse)
(;Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000
(;Accession: F30535
R;Claflin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.
J. Immunol. 138, 3060-3068, 1987
A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with A;Reference number: A30556; MUID:87196439; PMID:3106498
A;Accession: F30535
                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-107 <CLA>
A;Residues: 1-107 <CLA>
A;Cross-references: UNIPARC:UPI0000176AF9
A;Note: the sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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A;Note: the sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
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J. Immunol. 138, 3060-3068, 1987
A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced A;Reference number: A30556; MUID:87196439; PMID:3106498
A;Accession: D30535
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A;Molecule type: DNA
A;Residues: 1-107 <CLA>
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C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 16-Aug-1996
C;Accession: D30535
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93.5%;
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Pred. No. 3.8e-27;
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Pred. No. 2.4e-27;
                                                       Score 520; DB 2; I
Pred. No. 6.8e-27;
5; Mismatches 3;
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Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C; Species: Mus musculus (house mouse)
C; Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change
C; Accession: A56446
R; Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A; Title: A high affinity digoxin-binding protein displayed on M.
A; Reference number: A56446; MUID:95229583; PMID:7713873
A; Accession: A56446
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-268 < TANP
A; Cross-references: UNLPARC: UPI000017C6D0; GB:U20617
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A;Residues: 1-107 <CLA>
A;Cross-references: UNIPARC:UPI0000176AF5
A;Note: the sequence was determined from the differentiated gene C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;16-96/Domain: immunoglobulin homology <IMM>
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J. Immunol. 138, 3060-3068, 1987
A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced A;Reference number: A30556; MUID:87196439; PMID:3106498
A;Accession: B30535
A;Accession: B30535
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C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change
C;Accession: B30535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: heterotetramer; immunoglobulin
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Best Local Similarity
                                                                                                                                                                                                                                                                                   133 LEOSGAELVRPGTSVKISCKASGYAFTNYWLGWVKORPGHGLEWIGDIFPGSGNIHYNEK 192
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                                                -----SGGGGSDIKLQQSGAEL-ARPGASVKMSCK-TSGYTFTRYTMHWVKQRPGQGL 298
                                                                                                            FQGKATIAADTSSNTAYLQLSSLTSEDTAVYYCASYYLTRYE---NYMGQGTTVTVSSGG 122
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45; Mismatches 62
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6; Mismatches 3
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Search completed: March 6, 2006, 13:14:48 Job time : 26 secs	5.10
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Similarity 90.5%; Pred. No. 4.5e-26; 5; Conservative 7; Mismatches 3; ELYMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYL ::	- 0
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R;Claflin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W. J. Immunol. 138, 3060-3068, 1987 J. Immunol. 138, 3060-3068, 1987 A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced wit A;Reference number: A30556; MUID:87196439; PMID:3106498 A;Accession: C30535 A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA	
RESULT 15 C30535 Ig kappa chain V region (2B2) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000 C;Accession: C30535	000H0%
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ALIGNMENTS	Q7TMK1_MOUSE Q924P5_MOUSE	Q924R2_MOUSE	Q924R3_MOUSE	Q924Q4_MOUSE	HV11_MOUSE	Q924P7_MOUSE	Q8VCX7_MOUSE	HV01_MOUSE	Q6PF95_MOUSE	KV4C_HUMAN	Q99LC4_MOUSE	Q8K172_MOUSE	Q924R6_MOUSE
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RESULT 1 Q65ZI1 MOUSE PRELIMINARY; ID Q65ZI1, AC Q65ZI1; DT 25-OCT-2004 (TrembLrel. 28, Cr DT 25-OCT-2004 (TrembLrel. 28, La DT 25-OCT-2004 (TrembLrel. 28, La Query Match Best Local Similarity Matches 132; Conserv Z5-OCT-2004 (TrEMBLrel. 28, Last sequence update) Anti-HIV-1 reverse transcriptase single-chain variable. Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. [1] InterPro; IPR003599; Ig. InterPro; IPR007110; Ig-like. InterPro; IPR003598; Ig_c2. InterPro; IPR003598; Ig_c2. InterPro; IPR003596; Ig_v. SMART; SM00409; IG; 2. SMART; SM00408; IGc2; 2. SMART; SM00406; IGv2; 2. SMART; SM00406; IGv2; 2. PROSITE; PS50835; IG_LIKE; 2. Immunoglobulin domain; RNA-directed DNA polymerase. Immunoglobulin domain; RNA-directed DNA polymerase. SEQUENCE 262 AA; 27842 MW; 7DF20138E53865E4 CRC64; TISSUE-Hybridoma; MEDLINB-96211469; PubMed=8648670; MEDLINB-96211469; PubMed=8648670; Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.; Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.; "Targeting human immunodeficiency virus type 1 reverse transcripta by intracellular expression of single-chain variable fragments to by intracellular expression of single-chain variable fragments to inhibit early stages of the viral life cycle."; J. Virol. 70:3392-3400(1996). EMBL; U48716; AAB64342.1; -; mRNA. EMRE, 065211; 2-132. NUCLEOTIDE SEQUENCE. GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA 116 VSIFPPSSKLGPGGGGSGGGSGGGSELGRSEVQ-LQESGPSLVKPSQTLSLTCSVTGD 56 ISGIPSRFSGSGSGSDFTLSINSVEPEDVGVYYCQNGHSFPLTFGAGTKLELKRADAAPT 61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIK-----ELVMTQSPSSLTYTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR :::|||||::|:||::||::||::||::||::|| ELVMTQSPATLSVTPGDRVSLSCRASQSI-----SDFLHWYQQKSHESPRLLIKYASQS Conservative 32.6%; Score 666.5; DB 2; Length 262; 48.4%; Pred. No. 6.1e-42; cive 58; Mismatches 46; Indels 37 PRT; 262 ጅ transcriptase 37; Gaps 174 156 113 55

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175

SITSGYWNWIRKFPGNKLDYMGYI-NYSGDTYYNPSLKSRISITADTSKNQYYLQLNSVT 233

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QGKB05_MOUSE PRELIMINARY;
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05-UUL-2004 (TrEMBLrel. 27, Las
05-UUL-2004 (TrEMBLrel. 27, Las
ScFv B855 protein (Fragment).
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MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
Peter J.C., Eftekhari P., Billiald P., Wallukat G., Hoebeke J.
Peter J.C. single chain antibody variable fragment as inverse agoni
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01-OCT-2003 (TrEMBLrel. 25, I
01-MAR-2004 (TrEMBLrel. 26, I
SCFV 6H8 protein (Fragment).
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QTTQM2;
01-OCT-2003 (TrEMBLrel. 2
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 2.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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SMR; Q7TQM2; 1-236.
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J. Biol. Chem. 278:36740-36747(2003).
EMBL; AJ574851; CAE00495.1; -; Genomic
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MOUSE
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Pred. No. 1.9e-34;
13; Mismatches 71;
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SWART; SM00406; IGV; 2.
PROSITE; PS50835; IG_LIKE;
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Briand J.P., Hoebeke J.;
"Modulation of the M2 muscarinic acet:
monoclonal anti-M2 receptor antibody
J. Biol Chem. 279:55697-55706 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Monoclonal anti-idiotypic Schistosoma japonicum anti-chain variable region (Fragment).
Mus musculus (Mouse).
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NON TER
SEQUENCE
                                                                                                                                                                                     PROSITE;
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Song X.T., Feng Z.Q., Guan X.H.;

"Amplification, cloning and sequence analysis of the heavy variable region gene of monoclonal anti-idiotypic antibody Schietosoma japonicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodent
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9GYZ2 MOUSE PRELIMINARY;
Q9GYZ2;
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HSSP; P01837; 1KCR.
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HSSP; P01751; 1A6W.
SMR; Q9GYZ2; 1-119.
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InterPro; IPR003596;
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E; PS50835; IG
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96; Ig_v.
[Gv; 1.
IG_LIKE; 1.
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5; Mismatches
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   Score 527; DB 2;
Pred. No. 6.8e-32;
.2; Mismatches 13
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Pred. No. 1
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Q4KML5;
13-SEP-2005 (
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13-SEP-2005
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                                                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 617 AA; 6
                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2005) to the EMI EMBL; BC098504; AAH98504.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6NCr; I
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TSVTVSS
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                                    TTLTVSS
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  141
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                                                                                                                                                                                                                                                                                                                68520 MW;
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78.7%;
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Last annotation updat
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                                                                                                                                                                                                                                       Mismatches
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No. 8e-31;
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RESULT

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Q65ZL2_9MURI
ID Q65ZL2;
AC MAMBAIA; Eutheria; Euarcho QC Muroidea; Muridae; Murinae;
AC Eukaryota; Metazoa; Chordat QC Eukaryota; Muridae; Murinae;
AC MUROIdea; Muridae; Murinae;
AC MUROIDEA; Muridae; Murinae;
AC MUROIDEA; AC MURINAE;
AC MUROIDEA; AC MURINAE;
AC MUROIDEA; AC MUROIDEA;
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RESULT 7

Q52L64 MOUSE
ID Q52L64, MOUSE PRELIMINARY;
AC Q52L64,
DT 13-SEP-2005 (TrEMBLrel. 31,
DT 13-SEP-2005 (TrEMBLrel. 31,
DT 13-SEP-2005 (TREMBLrel. 31,
DT 13-SEP-2005 (TREMBLREL. 31,
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordat
OC Mammalia; Eutheria; Euarcho
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InterPro; IPR003599; IS.
InterPro; IPR003597; IS_C1.
InterPro; IPR003597; IS_C2.
InterPro; IPR003598; IS_C2.
InterPro; IPR003596; IS_MIC.
InterPro; IPR003096; IS_MIC.
InterPro; IPR003596; IS_VAC.
INTERPRO; IPR003596; IS_VAC.
INTERPRO; IPR003596; IS_VAC.
INTERPRO; IRR01396; IS_C2.
INTERPRO; INCO, IN
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MEDLINE=96272580; PubMed=8688499;
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Muroidea; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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           Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Euarchontoglires;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YYCOHFWGTPYT---FGGGTRLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YYCARYYDDHYCLDYWGOGTTLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.3%;
nilarity 46.2%;
Conservative 3
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(TrEMBLrel. 28, Last sequence up)
(TrEMBLrel. 28, Last annotation)
                                                Chordata;
                                                                                                                                                       31,
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                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                              Created)
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Pred. No. 1.8e-30;
5; Mismatches 63
                  Craniata; Vertel
oglires; Glires;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C7BAB69F30555504 CRC64;
                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370
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                                                                                                                                                                                                                                                                                                        240
                  Vertebrata; Euto
lires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                       Euteleostomi;
                      Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SYYGHWGQGTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Q569W9
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                                    RESULT 8
Q569W9_MOUSE
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RC TISUE-Hammary tumor. WAP-TGF alpha model. 7 months old;

RX MEDLINE-22388257; PubMed-12477932; DOI-10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,

RRA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RRA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RRA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RRA Bieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RRA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RRA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RRA Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,

RRA Robards S., Hoguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RRA Rohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RRA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RRA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RRA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RRA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RRA Rodriguez S., C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
Q569W9_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPRO07110; Ig-11ke.
InterPro; IPRO03597; Ig_Cl.
InterPro; IPRO03596; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; Cl-sec; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical SEQUENCE 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Mix FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Mammary t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Mix FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q52L64; 21-240.
                                                                                                                                                             166
                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity
112; Conser
                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             μ
                                                                                                                                                                                                                                                                                                                                   GGSGGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                            ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG
                                                                                                                                                                                                                 FPGSGNIHY----FEDSAVYFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSYNQKNYLAWYQQKPGQSPKLLIYWASTR
                                                                                                                                                      YPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTC
                                                                                                                                                                                                                                                                           --RADAAPTVSIFPPSSEQLTSGGASV---
                                                                                                                                                                                                                                                                                                                                                                                             ESGVPDHFSGSGSGTDFTLTISSVKAEDLALYYCQQYYNYPLTFGAGTKLDLR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (APR-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 AA; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
            PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26609 MW; CF8630CCC002E52C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 508.5; DB Pred. No. 4e-30;
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
            468
            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
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                                                                                                                                                                                                                                                                               -----VCFLNNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45;
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                                                                                                                                                                                                                 225
                                                                                                                                                         220
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RX MEDLINE=22388257; pubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley N.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butkesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RGeneration and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003596; Ig-wc.
InterPro; IPR003596; Ig-wc.
InterPro; IPR003596; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q569W9;
10-MAY-2005
10-MAY-2005
10-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUDMITTED (APR-2005) to the EMBL/GenBank/DDBJ databases EMBL; BC092271; AAH92271.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical SEQUENCE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CZECH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMR; Q569W9; 20-464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MGI:96443; Igh-la.
GO:0003823; F:antigen
                                                                                                                                                              183
                                                                                   73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Project;
                                                                                                                                             GSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRUMDEPMDYWGQGT
                                                                                                                                                                                                                                                                                       SGGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDIFP 182
    TVTVSSGGGGSDIKLQQSGAELARP----
                                                                                                                                                                                                                                         TAGVHSEVQ-LQQSGAELVRPGSSVKLSCKTSGYTFTSYYINWVKQRPGQGLEWIGHIYP
                                                                                   GNGYTEYNEKFKGKATLTSDTSSSTAYMQLRSLTSENSAIYFCARTGGYDGYFDYWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468
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RESULT 10
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P01746;
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Somatic mutation in genes for the variable immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=82152818; PubMed=6801765;
Sims J., Rabbitts T.H., Estess P.,
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21-JUL-1986 (Rel. 01, La
10-MAY-2005 (Rel. 47, La
Ig heavy chain V region
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on 93G7 precursor.
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RESULT 11
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurogna
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21-JUL-1986 (Rel. 01, Last sequence up.
13-SEP-2005 (Rel. 48, Last annotation Ig heavy chain V region 36-65.
                     MOUSE STANDARD; PRT; 139 AA PO1751; P01752; CRel. 01, Created)
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation updat Ig heavy chain V region B1-8/186-2 precurso Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genetic basis of antibody production: the dominant idiotype response of the strain A mouse."; Eur. J. Immunol. 12:1023-1032(1982).
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MEDLINE=83131846; PubMed=6:
Siekevitz M., Gefter M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A94264; HVMSG7.
PDB; 1JFQ; X-ray; H=1-120.
Ensembl; ENSMUSG00000021155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Parhami-Seren B.,
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PROSITE; PS50835; IG LIKE; 1.

3D-structure; Hybridoma; Immunoglobulin
Immunoglobulin V region.
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InterPro; IPR003596; Ig_v.
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Pred. No. 8.7e-30;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;

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Query Match
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Matches 95
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PDB; IAGW; X-ray; H/1/J=20-139.

PDB; IAGW; X-ray; H=20-139.

PDB; INGP; X-ray; H=20-139.

PDB; INGQ; X-ray; H=20-139.

PDB; INGQ; X-ray; H=20-139.

PDB; INGB; X-ray; A/C=20-139.

Ensembl; ENSMUSGO000063737; Mus musculus.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A90809; MHMS18.
PDB; 1A6U; X-ray; H-2
PDB; 1A6W; X-ray; H-2
PDB; 1A6W; X-ray; H-2
PDB; 1NGP; X-ray; H-2
PDB; 1NGB; X-ray; H-2
PDB; 1NGB; X-ray; A/C
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Cell 24:625-637(1981)
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[1]
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Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=81234548;
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3D-structure; Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s Swiss-Prot entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L 24:625-637(1981).
MISCELLANEOUS: The B1-8 mu chain mRNA was cloned from a hybridoma
making antibodies to the hapten (4-hydroxy-3-nitrophenyl)acetyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NPb antibodies).
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           Similarity
  Conservative
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Paskind M., Reth
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                                         15419 MW;
          23.9%;
72.0%;
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          Score 489.5;
Pred. No. 5.4
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Framework-3.
D segment.
UH2 segment.
By similarity.
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                                        1B57DD4FD0C9F465 CRC64;
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 Mismatches
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M., Imanishi-Kari T., Rajewsky K.
                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin V region; Signal.
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences ",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
Query Match
                                                                                                         Submitted (MAY-2005) to the EMBL/GenBai
EMBL; BC096667; AAH96667.1; -; mRNA.
MGI; MGI:96448; Igh-6.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig. 1
InterPro; IPR003597; Ig. cl.
InterPro; IPR003597; Ig. cl.
InterPro; IPR003006; Ig. MHC.
InterPro; IPR003906; Ig. V.
Pffam; PF07654; Cl.=8et; 4.
SMART; SM00407; IGC1; 4.
SMART; SM00407; IGC1; 4.
SMART; SM00406; IGV; I.
PROSITE; PS00835; IG_LIKE; 5.
PROSITE; PS00835; IG_MHC; UNKNOWN_3.
                                                           Hypothetical protein 
SEQUENCE 590 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Mammary gland;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Gro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musiae; Mus.
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13-SEP-2005 (TrEMBLrel.
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                                                           64892 MW; D425318F9A188B14 CRC64;
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23.9%; Score 489;
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Last annotation update)
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ID Q924R0 MOUSE
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Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989)

EMBL; AB067790; BAB63275.1; -; mRNA.

PIR; F28833; F28833.

PIR; F33932; F33932.

PIR; P31932; P31932.

PIR; P3195; PH1105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
VH186.2-D-J-C mu protein (Fragment).
Name=VH186.2-D-J-C mu;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.; "Allogeneic manipulation of the GAT idiotypic cascade. Immunization C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-specific V genes as the original antigen."; Immunol. 141:779-784(1988).
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Q924R0;
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"Two murine natural polyreactive autoantibodies are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Euarchont
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Last annotation update)
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EMBL/GenBank/DDBJ
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Q924P8_MOUSE
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SMR; Q954R0; 1-134.
InterPro; IPR007110;
InterPro; IPR003596; J
SMART; SM00406; IGV; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-OCT-2003 (TrEMBLel. 25, Last annotation
V23-D-J-C mu protein (Fragment).
Name=AB069917; Synonyms=V23-D-J-C mu;
Nus musculus (Mouse).
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Q924P8;
01-DEC-2001 (
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NON_TER
SEQUENCE
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Submitted (AUG-2001)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                          PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corbet S., Hirn M., Roth C., Theze J., Fougereau "Allogeneic manipulation of the GAT idiotypic car C57BL/6 mice by BALB/c anti-idiotypes stimulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6;
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                                                                                                                                                                                                                               SMART; SM00406;
                                                                                                                                                                                                                                                                                                                                                                                                                                               specific
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
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mmunol. 141:779-784(1988).
,, AB069917, BAB63933.1; -; mRNA.
128833; 128833.
PH1156; PH156.
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Q924P8; 1-126.
MGI:3576502; AB069917
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93; Conservative
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IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYN
                                                                                                                                                                                                           PS50835;
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143 AA;
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140 AA;
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15392 MW;
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co the EMBL/GenBank/DDBJ databases.
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Pred. No. 9.
                                                          6
                                                            Score 485; DB 2;
Pred. No. 1.2e-28;
6; Mismatches 15
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lotypic cascade.
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e. Immunization
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BL4_MOUSE
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Q9D8L4;
01-JUN-2001 (
01-JUN-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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01-JUN-2001 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
library, clone:1810060009 product:immunoglobulin heavy chain 6 (heavy
                                                                                                                                              Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Pancreas; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
   STRAIN=C57BL/6J; TISSUE=Pancreas; MEDLINE=20530913; PubMed=11076861;
                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE-Pancreas; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wynshaw-Boris A
Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Pancreas;
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STRAIN=C57BL/6J; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of Nature 409:685-690(2001).
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                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FANTOM Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Pancreas;
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   DOI=10.1101/gr.152600;
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A Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

A Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Sakai C., Sakai K.,

A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai R.,

A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

A Sogabe Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

A Muramatsu M., Hayashizaki Y.,

A Muramatsu M., Hayashizaki Y., Bhill, F., Tanaki T.,

Bull, AKOO7918; BAB25349.1; -; mRNA.
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PIR; S19966; S19966.

PIR; S26746; S26746.

RSSP; PD1864; 1BOG.

SMR; Q9BEL4; 20-469.

Ensembl; ENSMUSG00000054328; Mus musculus.

MGI; MGI:96443; Igh-La.

GO; GO:0005771; C:multivesicular body; IDA.

GO; GO:0005771; C:multivesicular body; IDA.

GO; GO:0001788; F:antigen binding; IDA.

GO; GO:0001788; P:antigen processing; IDA.

GO; GO:0006931; P:enaly endosome to late ender colored colore
                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF07654; C1-set;
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                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p; IPR007110; Ig-like.
p; IPR003597; Ig c1.
p; IPR00306; Ig_MHC.
p; IPR003596; Ig_MHC.
p; IPR003596; Igv.
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GSGSTYYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGYDYDWFAYWGQGT
                                                           GSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQGT
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Prositive regulation of immune response; IDA.
Prositive regulation of phagocytosis; IDA.
Prositive regulation of type I hypersensitivity; IDA.
Prositive regulation of type IIa hypersensit. . .; ID.
Prositive regulation of type IIa hypersensit. . .; ID.
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P:complement activation, classical pathway; IDA.
P:early endosome to late endosome transport; IDA
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P:antibody-dependent cellular cytotoxicity; IDA.
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Pred. No. 5.3e-28;
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7: /cgn2_6/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-495-664-3
US-11-116-939-11
US-11-116-939-10
US-11-116-939-10
US-11-0981-256A-29
US-11-0981-244-21
US-11-0984-9558-29
US-11-0984-9558-23
US-11-0984-9558-25
US-11-0981-356A-26
US-11-0981-356A-26
US-11-0981-356A-27
US-11-0981-356A-28
US-11-0981-356A-29
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US-10-495-664-3
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Best Local &
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Result

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519	519	521	522	524	526.5	527	528.5	529.5	529.5	533	553	558	562.5	585.5	600	602	609.5	612.5	630
25.4	25.4	25.5	25.5	25.6	25.7	25.8	25.8	25.9	25.9	26.1	27.0	27.3	27.5	28.6	29.3	29.4	29.8	29.9	30.8
119	119	263	328	252	248	113	277	277	249	241	113	113	248	319	290	615	317	226	119
7	7	σ	7	7	σ	7	7	7	7	σ	7	7	σ	7	7	σ	σ	7	7
US-11-221-900-14	US-11-221-900-13	US-10-512-184-29		US-11-054-515-1537	US-10-512-184-36	US-11-076-395-16	US-11-126-817-54	US-11-126-817-52	US-11-201-825-24	US-10-902-546-6	US-11-076-395-45	US-11-076-395-46	US-10-512-184-32	US-11-032-773-955	US-11-032-773-957	US-10-512-184-50	US-10-512-184-69	US-11-183-205-42	US-11-221-900-10
Sequence 14, Appl	Sequence 13, Appl	Sequence 29, Appl		. 5			4.	٠			Sequence 45, Appl	4 6		9 0	957	,	6,6	42,	Sequence 10, Appl

ALIGNMENTS

Sequence 3, Application US/10495664 Publication No. US20050244416A1 GENERAL INFORMATION: SOFTWARE: PatentIn Ver. 3.3 SEQ ID NO 3 LENGTH: 543 CURRENT APPLICATION NUMBER: US/10/495,664 CURRENT FILING DATE: 2004-05-12 PRIOR APPLICATION NUMBER: PCT/EP02/12545 PRIOR FILING DATE: 2002-11-09 PRIOR APPLICATION NUMBER: DE 101 56 482.1 PRIOR APPLICATION NUMBER: DE 101 56 482.1 PRIOR FILING DATE: 2001-11-12 NUMBER OF SEQ ID NOS: 3 APPLICANT: JUNG, GUNDRAM TITLE OF INVENTION: BISPECIFIC ANTI-CD28 ANTIBODY MOLECULE FILE REFERENCE: 034258-0801 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: protein construct TYPE: PRT ORGANISM: Artificial Sequence FEATURE: y Match 55.3%; Local Similarity 56.7%; hes 224; Conservative 59 21 DIVLTQSPASLAVSLGQRATISCRASESV-----EYYVTSLMQWYQQKBGQPPKLLIFA ASTRESGVPDRFTGSGSGTDFTUTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIK-GG ; Score 1130.5; DB 6; ; Pred. No. 2.2e-64; 59; Mismatches 81; 81; Indels Length 31; Gaps

PMDYWGQGTTVTVS-----SGGGGSDIKLQQSGAELARPGASVKMSCKTSG WLGVIWAGGGT-NYNSALMSRKSISKDNSKSQVFLKMNSLQADDTAVYYCARDKGYSYYY

SMDYWĠQĠŢŢŶŢŶŚSASTKGPSVFPLAPŚSSĠSGQVKĹQQŚĠPĖĹVKPĠAŚVKIŚCKAŚĠ

312

279

GGSGGGSGGGSQVK-LQQSGPGLVTPSQSLSITCTVSGFSLSDYGVHWVRQSPGQGLE GGSGGGSGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLE ASNVESGVPARFSGSGSGTNFSLNIHPVDEDDVAMYFCQQSRKVPYTFGGGTKLEIKRGG

175

134

74

8

WIGDIFPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWD--E

252

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APPLICANT: Stephen Tomlinson
APPLICANT: Richard J. Quigg
TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
FILE REFERENCE: 19113.0115U2
CURRENT APPLICATION NUMBER: US/11/116,939
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: 60/565,907
PRIOR FILING DATE: 2004-04-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 824
TYPE: PRT
ORGANISM: Artificial Sequence
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US-11-116-939-11
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Publication No. US20050265995A1
GENERAL INFORMATION:
                                                                                       Sequence 12, Application US/11116939 Publication No. US20050265995A1 GENERAL INFORMATION:
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Best Local Similarity
         APPLICANT: Stephen Tomlinson
APPLICANT: Richard J. Quigg
TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT
FILE REFERENCE: 19113.0115U2
CURRENT APPLICATION NUMBER: US/11/116,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GGSGGGG-------SEVQLLEQSGAELVRPGTSVKISCKASGYAFTNY 161
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Pred. No. 1.4e-55;
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APPLICANT: Stephen Tomlinson
APPLICANT: Richard J. Quigg
APPLICANT: Richard J. Quigg
FILE REFERENCE: 19113.0115U2
CURRENT APPLICATION NUMBER: US/11/116,939
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: 60/565,907
PRIOR APPLICATION NUMBER: 60/565,907
PRIOR FILING DATE: 2004-04-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
SEQ ID NO 10
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US-11-116-939-10
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PRIOR APPLICATION NUMBER: 60/565,907
PRIOR FILING DATE: 2004-04-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/11116939 Publication No. US20050265995A1
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Best Local Similarity
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                  Query Match
Best Local
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TYPE: PRT
ORGANISM: Artificial S
FEATURE:
                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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OTHER INFORMATION:
                                                                             OTHER INFORMATION: Description OTHER INFORMATION: construct
                                                                                                            FEATURE:
                                                                                                                                                           LENGTH:
                  Local Similarity
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191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR
                                                                                                                                                             293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WLGWVKQRPGHGLEWIGDIFPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSA
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        46.8%;
70.2%;
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Score 958.5; DB 7; Pred. No. 8.2e-54; 20; Mismatches 34
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Pred. No. 8.6e-56;
                                                                                             of Artificial Sequence; note-synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Artificial Sequence; note=synthetic
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                               DB 7;
 34;
                                                                                                                                                                                                                                                                                                        MODULATORS
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 Indels
                                293;
27;
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Sequence 29, Application US/10981356A

Publication No. US20060015952A1

GENERAL INFORMATION:
APPLICANT: FILVANOFF, ELLEN H.

ITILE OF INVENTION: SCREENING ASSAYS AND METHODS OF INTERFERENCE: P2066R1

CURRENT APPLICATION NUMBER: US/10/981,356A

CURRENT FILING DATE: 2004-11-04

PRIOR APPLICATION NUMBER: US 60/520,398

PRIOR FILING DATE: 2003-11-13

PRIOR APPLICATION NUMBER: US 60/57,951

PRIOR FILING DATE: 2003-03-11

UNUMBER OF SEQ ID NOS: 45

SEQ ID NO 29

LENGTH: 666
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US-10-981-356A-29
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-10-981-356A-29
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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les 209; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYYCARPNNYGSSPPYYAMDCWGQGTSVTVSS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYFCARLRNWDE-----PMDYWGQGTTVTVSS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIHWVKQSHAKSLEWIGVISTYYGHTHYNQKFKGKATLTVDKSSNTAYMELARLTSEDSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WLGWVKQRPGHGLEWIGDIFPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĠĠŚĠĠĠĠŚMGWŚCVMLFLVATATGVHŚQVQ-ĹEQŚĠPĒĹVRPGVSVKISCKGSGYTFTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG
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                                                                                                                                                        DYWGQGTTVTVSSGGGGSDIKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPG
                                                                                                                                                                                       ALQSGN-----SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC-----EV
                                                                                                                                                                                                                                                                                                                                                                                   FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLT----FEDSAVYFCARLRNWDEPM
                                                                                                                                                                                                                                                        --RTVAAPSVFIFPPSDEQL-KSGTA-SVVC-----LLNNFYPREAK-----VQWKVDN
                                                                                                                                                                                                                                                                                     GGSGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDI 180
                                                                                                                                                                                                                                                                                                                                         ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG
                            HYCLDYWGOGTTLTVSS 372
                                                                                            QGLEWIGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDD
                                                                                                                          THQGLSSPVTKSFNRGECEVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPG
                                                                                                                                                                                                                                                                                                                      ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYC-HQYLSSDTFGGGTKLEIK-----
GFYFDYWGQGTSVTVSS 336
                                                            46.5%; Score 952; DB 6; ilarity 55.4%; Pred. No. 4.2e-53; Conservative 36; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence is synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SEVQLLEQSGAELVRPGTSVKISCKASGYAFTNY 161
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RESULT 7 US-11-084-717-21

Sequence 21, Application US/11084717
publication No. US20050260736A1
GENERAL INFORMATION:
APPLICANT: GEORGIOU, GEORGE
APPLICANT: JEONG, KI-JUN
APPLICANT: HARVEY, BARRETT R.

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APPLICANT: PRESTA, LEONARD G.
APPLICANT: TEJADA, MAX L.
TITLE OF INVENTION: Humanized Anti-TGF-Beta Ant
FILE REFERENCE: P1954RIUS
CURRENT APPLICATION NUMBER: US/11/096,046
CURRENT FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: US 60/558,290
PRIOR FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 29
LENGTH: 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 220
; OTHER INFORMATION: U
US-11-096-046-29
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Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ADAMS, CAMELLIA W.
APPLICANT: FERRARA, NAPOLEONE
APPLICANT: FILVAROFF, ELLEN H.
APPLICANT: MAO, WEIGUANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKUYLTWYQQKPGQPPKLLIYWASTR
                                                                                                                                                THOGLSSPYTKSFNRGECXEVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRP
                                                                                                                                                                                DYWGQGTTVTVS-SGGGGSDIKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRP
                                                                                                                                                                                                                       ALQSGN-----SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC-----EV
                                                                                                                                                                                                                                                                                                                                                                                          ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG
GGFYFDYWGQGTSVTVSS 337
                                    DHYCLDYWGOGTTLTVSS 372
                                                                                                         GOGLEWIGYINPSRGYTNYNOKFKDKATLTTDKSSSTAYMOLSSLTSEDSAVYYCARYYD
                                                                                                                                                                                                                                                         FPGSGNIHYNEKFKGKATLTADKSSSTAYMOLSSLT----FEDSAVYFCARLRNWDEPM
                                                                                                                                                                                                                                                                                                  --RTVAAPSVFIFPPSDEQL-KSGTA-SVVC-----LLNNFYPREAK------VQWKVDN
                                                                                                                                                                                                                                                                                                                                                                             ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYC-HQYLSSDTFGGGTKLEIK------
                                                                       GQGLEWIGVNNPGSGGSNYNEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR--S
                                                                                                                                                                                                                                                                                                                                    GGSGGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.1%; Score 942.5; DB 7
55.3%; Pred. No. 1.7e-52;
tive 37; Mismatches 85
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120 60

294

261

235 157

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PRIOR APPLICATION NUMBER: 60/554,324
PRIOR PILING DATE: 2004-03-18
PRIOR PILING DATE: 2003-07-15
PRIOR PILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,058
PRIOR PILING DATE: 2002-07-15
PRIOR PILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 21
LENGTH: 247
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-11-179-244-21
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US-11-179-244-21
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Matches
                                                                                                                               SEQ ID NO 21
LENGTH: 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21, Application US/11179244
Publication No. US20050267294A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                         APPLICANT: HARVEY, BARRETT R.
APPLICANT: GEORGIOU, GEORGE
APPLICANT: IVERSON, BRENT L.
TITLE OF INVENTION: ANTIBODIES WITH INCREASED AFFINITIES FOR ANTHRAX ANTIGENS
FILE REFERENCE: UTSB: 721US
CURRENT APPLICATION UMBER: US/11/179,244
CURRENT FILING DATE: 2005-07-12
PRIOR APPLICATION NUMBER: US/10/620,049
PRIOR FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,058
PRIOR FILING DATE: 2002-07-15
UNDBER OF SEQ ID NOS: 25
UNDBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: IVERSON, BRENT L.
TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES
FILE REFERENCE: UTSB:723US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/11/084,717
CURRENT FILING DATE: 2005-03-18
                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.1
                OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Peptide
                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 167; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTPGAGTKLEIK-----G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDYWGQGTTVTVSS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EWIGRIYPGDGDTNYNGKFKGKATLTÄDKSSSTAYMQLSSLTSVDSAVYFCARSGLLRYA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EWIGDIFPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGSGGGGSGGGSEVQ-LQQSGPELVKPGASVKISCKDSGYAFSSSWMNWVKQRPGQGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIQMTQTTSSLSASLGDRVTISCRASQDI-----RNYLNWYQQKPDGTVKLLIYYTSRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247
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; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: Peptide US-11-084-055B-21
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US-11-084-055B-21
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CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/554,260
PRIOR FILING DATE: 2004-03-18
PRIOR PRIOR DATE: 2004-03-18
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 21
LENGTH: 247
TYPET - THE TABLE PATENTIN THE TABLE PATENT THE TABLE PAT
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APPLICANT: GEORGIOU, GEORGE
APPLICANT: JEONG, KI JUN
APPLICANT: IVERSON, BRENT L.
APPLICANT: IVERSON, BRENT L.
APPLICANT: IVERSON, BRENT L.
APPLICANT: IVERSON, BRENT L.
TITLE OF INVENTION: COMBINATORIAL PROTEIN LIBRARY
TITLE OF INVENTION: PERIPLASMIC EXPRESSION
FILE REFERENCE: UTSB:722US
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Best Local Similarity 65.7
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/11084055B Publication No. US20060029947A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                    61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIK-----G
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   MDYWGQGTTVTVSS 248
                                                                                                                            EWIGDIFPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEP
                                                                     EWIGRIYPGDGDTNYNGKFKGKATLTADKSSSTAYMQLSSLTSVDSAVYFCARSGLLRYA 233
                                                                                                                                                                                                     GGGSGGGGGGGGSEVQ-LQQSGPELVKPGASVKISCKDSGYAFSSSWMNWVKQRPGQGL
                                                                                                                                                                                                                                                                                                                                  QSGVPSRFSGSGSGTDYSLTISNQEQEDIGTYFCQQGNTLPWTFGGGTKLEIKRGGGGSG
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CURRENT APPLICATION NUMBER: US/11/084,717
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/554,324
PRIOR FILING DATE: 2004-03-18
PRIOR PRIOR APPLICATION NUMBER: 10/620,278
PRIOR FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,058
PRIOR APPLICATION NUMBER: 60/396,058
PRIOR PILING DATE: 2002-07-15
UNMBER OF SEQ ID NOS: 61
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 23
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                                                                                                                                                                                                                                                                                      RESULT 11
US-11-179-244-23
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Sequence 23, Application US/11179244
Publication No. US20050267294A1
GENERAL INFORMATION:
APPLICANT: HARVEY, BARRETT R.
APPLICANT: GEORGIOU, GEORGE
APPLICANT: GEORGIOU, GEORGE
APPLICANT: GEORGIOU, BRENT L.
TITLE OF INVERTION: ANTIBODIES WITH INCREASED AFFINITIES FOR ANTHRAX ANTIGENS
FILE REFERENCE: UTSB:721US
CURRENT APPLICATION NUMBER: US/11/179,244
CURRENT FILING DATE: 2005-07-12
PRIOR APPLICATION NUMBER: US/10/620,049
PRIOR FILING DATE: 2003-07-15
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Best Local Similarity
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APPLICANT: JEONG, KI-JUN
APPLICANT: HARVEY, BARRIT R.
APPLICANT: IVERSON, BRENT L.
TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES
FILE REFERENCE: UTSB:723US
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                        MDYWGQGTSVTVSS
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Peptide
US-11-179-244-23
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SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 23
LENGTH: 247
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Best Local Similarity 63.4%;
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SEQ ID NO 23
LENGTH: 247
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Best Local Similarity 63.4%;
Matches 161; Conservative 33
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OTHER INFORMATION: Description
OTHER INFORMATION: Peptide
3-11-084-055B-23
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GEORGIOU, GEORGE
APPLICANT: JEONG, KI JUN
APPLICANT: IVERSON, BERNT L.
TITLE OF INVENTION: COMBINATORIAL PROTEIN LIBRARY SCREENING
TITLE OF INVENTION: PERLIPLASMIC EXPRESSION
FILE REFERENCE: UTSB: 722US
CURRENT APPLICATION NUMBER: US/11/084,055B
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/554,260
PRIOR APPLICATION SUMBER: 60/554,260
PRIOR APPLICATION SUMBER: 60/554,260
PRIOR FILING DATE: 2004-03-18
NUMBER OF SEQ. ID NOS: 59
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PRIOR FILING DATE: 2002-07-15
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    ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIK-----G 114
                                           DIQMIQITSSISASIGDRVIVSCRASQDI----RNYLNWYQQKPDGTVKFLIYYTSRL 54
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                                                                                                                         33; Mismatches
                                                                                                                                           Score 830.5; DB 7
Pred. No. 7.7e-46;
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RESULT 14
US-11-179-244-25
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LENGTH: 247
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Best Local
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APPLICANT: IVERSON, BRENT L.
APPLICANT: IVERSON, BRENT L.
APPLICANT: IVERSON, BRENT L.
APPLICATION INVESTIGATION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES
FILE REFERENCE: UTSS:723US
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/554,324
PRIOR FILING DATE: 2004-03-18
PRIOR FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: 10/620,278
PRIOR APPLICATION NUMBER: 10/620,278
PRIOR PILING DATE: 2002-07-15
PRIOR PILING DATE: 2002-07-15
PRIOR PILING DATE: 2002-07-15
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-11-084-717-25
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SOFTWARE: PatentIn Ver. 2.1
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Local Similarity 63.4%; Pred. No. 1.6e-45;
hes 161; Conservative 32; Mismatches 48
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                                                                                      MDYWGQGTSVTVSS 247
                                                                                                          MDYWGQGTTVTVSS 248
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  OTHER INFORMATION: Description of Artificial Sequence:
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APPLICANT: GEORGIOU, GEORGE

APPLICANT: JEONG, KIJUN

APPLICANT: JEONG, KIJUN

APPLICANT: JEONG, KIJUN

APPLICANT: JEONG, KIJUN

TITLE OF INVENTION: COMBINATORIAL PROTEIN LIBRARY SCREENING BY

TITLE OF INVENTION: PERIPLASMIC EXPRESSION

FILE REFERENCE: UTSB:772US

CURRENT APPLICATION NUMBER: US/11/084,055B

CURRENT FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: 60/554,260

PRIOR APPLICATION NUMBER: 60/554,260

PRIOR PILING DATE: 2004-03-18

NUMBER OF SEQ ID NOS: 59

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 25
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US-11-084-055B-25
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Best Local Similarity 63.4%; Pred. No. 1.6e-45;
Matches 161; Conservative 32; Mismatches 48
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PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 247
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Publication No. US20050267294A1
GENERAL INFORMATION:
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APPLICANT: IVERSON, BRENT L.
TITLE OP INVENTION: ANTIBODIES WITH INCREASED AFFINITIES FOR ANTHRAX ANTIGENS
FILE REFERENCE: UTSB:721US
CURRENT APPLICATION NUMBER: US/11/179,244
CURRENT FILING DATE: 2005-07-12
PRIOR APPLICATION NUMBER: US/10/620,049
PRIOR PILING DATE: 2003-07-15
PRIOR FILING DATE: 2003-07-15
PRIOR FILING DATE: 2003-07-15
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Peptide
TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                       LENGTH:
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Synthetic

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Query Match
Query Match
Best Local Similarity 63.4%; Score 825.5; DB 7; Length 247;
Best Local Similarity 63.4%; Pred. No. 1.6e-45;
Matches 161; Conservative 32; Mismatches 48; Indels 13; Gaps 3;
Matches 161; Conservative 32; Mismatches 48; Indels 13; Gaps 3;

Matches 161; Conservative 32; Mismatches 48; Indels 13; Gaps 3;

Pred. No. 1.6e-45;
Matches 161; Conservative 60; Indels 13; Gaps 3;

Matches 161; Conservative 61; Indels 13; Gaps 3;

Matches 161; Conservative 62; Indels 13; Gaps 3;

Matches 161; Conservative 62; Indels 13; Gaps 3;

Matches 161; Conservative 62; Indels 13; Indels
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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1189.5
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   6.5.4.2.2.
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US-10-682-845-63
US-10-682-845-63
US-10-682-845-73
US-10-682-845-73
US-10-682-845-73
US-10-682-845-75
US-10-682-845-79
US-10-682-845-81
US-10-682-845-81
US-10-805-177-113
US-11-336-098-18
US-10-239-656-47
US-10-296-085A-17
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301 IGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLD

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US-09-948-004-18
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Sequence 18, Application US/10672932
Publication No. US20050191702A1
GENERAL INFORMATION:
APPLICANT: MACK, Matthias
TITLE OF INVENTION: Antibody and/or chemokine constructs and their use
TITLE OF INVENTION: immunological disorders
FILE REFERENCE: E 2411 EP
CURRENT APPLICATION NUMBER: US/10/672,932
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: US/09/948,004
PRIOR FILING DATE: 2001-09-05
NUMBER OF SEQ ID NOS: 34
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Publication No. US20030017979A1
GENERAL INFORMATION:
APPLICANT: MACK, Matthias
TITLE OF INVENTION: Antibody and/or chemokine constructs and their use
TITLE OF INVENTION: immunological disorders
FILE REFERENCE: E 2411 EP
CURRENT APPLICATION UMMBER: US/09/948,004
CURRENT FILING DATE: 2001-09-05
NUMBER OF SEQ ID NOS: 34
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SEQ ID NO 18
LENGTH: 495
TYPE: PRT
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APPLICANT: GREINER, AXEL
APPLICANT: BORKEN, BERNU
APPLICANT: BORKEN, BERNU
APPLICANT: BURGOU, RALF
APPLICANT: KUFER, PETER
TITLE OF INVENTION: ANTIBODIES AGAINST PLASMA CEI
FILE REFERENCE: 009848-0272298
CURRENT APPLICATION NUMBER: US/10/168,809
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: PCT/PP00/13238
PRIOR TILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: DE 199 62 583.2
PRIOR APPLICATION NUMBER: DE 199 62 583.2
PRIOR FILING DATE: 199-12-23
, ORGANISM: Artificial Sequence ; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic hybrid, ; OTHER INFORMATION: natural origin US-10-168-809-22
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US-10-168-809-22
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; ORGANISM: Mus
US-10-672-932-18
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                                                                                      NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 500
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22, Application US/10168809 Publication No. US20030180799A1
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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74.7%; Pred. No. 4.2e-91;
tive 34; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365
                                                                                                                                                                                                                                                                                                                                                                                                               Hans Konrad
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Query Match Best Local Similarity Matches 285; Conserv

Conservative

71.7%; Score 1467; DB 4; 76.4%; Pred. No. 6.2e-90;

DB 4;

Length 500 Indels

4.

Gaps

4

Mismatches

297

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RESULT 5
US-10-805-177-111
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/456,652
PRIOR FILING DATE: 2003-03-19
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 111
LENGTH: 499
TYPE: PRT
                                                                                                                                                                                                                                                                                       Query Match 70.4%; Score 1439.5; DB 5; Best Local Similarity 71.4%; Pred. No. 4.2e-88; Matches 270; Conservative 41; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mezes, Peter APPLICANT: Khramtsov, Nikolia APPLICANT: Khramtsov, Nikolia TITLE OF INVENTION: ANTHODIES AGAINST T CELL IMMUNOGLOBULIN TITLE OF INVENTION: DOWAIN AND MUCIN DOWAIN 1 (TIM-1) ANTIGEN AND USES FILE REFERENCE: ABXCUR.006A CURRENT APPLICATION NUMBER: US/10/805,177
CURRENT FILING DATE: 2004-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Landes, Gregory M.
APPLICANT: Chen, Francine
APPLICANT: Bezabeh, Binyam
APPLICANT: Foltz, Ian
APPLICANT: Tote, Kam Fai
                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Sapiens
-10-805-177-111
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GGSGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDI 180
                                                                                                            ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG 120
                                                                                                                                                                                     DIVMTQTPLSLPVTPGEPASISCRSSRSLLDSDDGNTYLDWYLQKPGQSPQLLIYTLSYR
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                                                                           ASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQRVEFPITFGQGTRLEIKGGGSGG
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Tse, Kam Fai
Jeffers, Michael
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Mezes, Peter
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TITLE OF INVENTION: Potent T cell modulating mol
FILE REFERENCE: G2296 US
CURRENT APPLICATION NUMBER: US/10/682,845
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.1
SEQ ID NO 59
LENGTH: 492
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-10-682-845-59
; Sequence 59, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 69.1%; Score 1414; DB 4; Length Best Local Similarity 71.2%; Pred. No. 2.1e-86; Matches 265; Conservative 43; Mismatches 54; Indels
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     YWGQGTTLTVSS
                                                                                                                                                                                                                                                                                               ## SG-GSTDYNAAFISRLSISKDNSKSQVFFKMNSLQANDTAIYYCARMENWS--FAYWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG
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                                                                                    IGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLD
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Gaps

180

173

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114

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60

360

300 230 240

290

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351

YWGQGTTLTVSS 362

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US-10-682-845-87
Sequence 87, Application US/10682845
Publication No. US20040162411A1
GENERAL INFORMATION:
APPLICANT: Lanzavecchia, Antonio
TITLE OF INVENTION: Potent T cell modulating molecules
FILE REFERENCE: G2296 US
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US-10-682-845-61
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CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR PILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.1
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LENGTH: 492
TYPE: PRT
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Publication No. US20040162411A1
GENERAL INFORMATION:
APPLICANT: Lanzavecchia, Antonio
TITLE OF INVENTION: Potent T cell modulating
FILE REFERENCE: G2296 US
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Best Local Similarity
Matches 264; Conserv
CURRENT APPLICATION NUMBER: US/10/682,845
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
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1 ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR 60

Conservative

43; Mismatches

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US-10-682-845-87
                                                                        OTHER INFORMATION: SCFV EDCAMXCD3 with M7 mutant in anti-CD3 US-10-682-845-65
Query Match
Best Local Similarity
Matches 264; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 65, Application US/10682845
Publication No. US20040162411A1
GENERAL INFORMATION:
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO 87
                                                                                                                                                                               NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65
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CURRENT APPLICATION NUMBER: US/10/682,845
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR FILING DATE: 2002-10-11
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lanzavecchia, Antonio TITLE OF INVENTION: Potent T cell modulating
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ORGANISM: artificial sequence
FEATURE:
                                                                                                                   TYPE: PRT ORGANISM: artificial sequence
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71.0%; Pred. No. 6.2e-86;
ative 44; Mismatches 54
                  68.7%;
 Score 1406; DB 4;
Pred. No. 7.2e-86;
3; Mismatches 55;
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Sequence 67, Application US/10682845

Publication No. US20040162411A1

GENERAL INFORMATION:
APPLICANT: Lanzavecchia, Antonio
TITLE OF INVENTION: Potent T cell modulating mol
FILE REFERENCE: G2296 US
CURRENT APPLICATION NUMBER: US/10/682,845
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.1
SEQ ID NO 67
LENGTH: 492
Type: DRT
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US-10-682-845-67
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    RESULT 12
US-10-682-845-71
; Sequence 71, Application US/10682845
; Publication No. US20040162411A1
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APPLICANT: Lanzavecchia, Antonio
TITLE OF INVENTION: Potent T cell modulating mol
FILE REFERENCE: G2296 US
CURRENT APPLICATION NUMBER: US/10/682,845
CURRENT FILLING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.1
SEQ ID NO 63
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US-10-682-845-63
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TYPE: PRT
ORGANISM: artificial sequence
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                            YWGQGTTLTVSS 372
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; Pred. No. 8.4e-86;
43; Mismatches 55;
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RESULT 13
US-10-622-845-69
; Sequence 69, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 71
SEQ ID NO 71
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APPLICANT: Lanzavechia, Antonio
TITLE OF INVENTION: Potent T cell modulating
FILE REFERENCE: G2296 US
                                                              SOFTWARE: PatentIn version 3.1 SEQ ID NO 69
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Best Local Similarity
                                                                                                   APPLICANT: Lanzavecchia, Antonio
TITLE OF INVENTION: Potent T cell modulating molecules
FILE REFERENCE: G2296 US
CURRENT APPLICATION NUMBER: US/10/682,845
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR FILING DATE: 2002-10-18
PRIOR FILING DATE: 2002-10-11
NUMBER: OF SEQ ID NOS: 89
RIOR FILING DATE: 2002-10-11
NUMBER: OF SEQ ID NOS: 89
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CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
LENGTH: 492
TYPE: PRT
ORGANISM: artificial sequence
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TYPE: PRT
ORGANISM: artificial sequence
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YSGVPDRFTGSGSGTDFTLTISNVQSEDLAEYFCQQYNSYPLTFGAGTKLEIKGGGGSGG

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APPLICANT: LARZAVECCHIA, Antonio
TITLE OF INVENTION: Potent T cell modulating mo:
FILE REFERENCE: 62296 US
CURRENT APPLICATION NUMBER: US/10/682,845
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR FILING DATE: 2002-10-11
JUNDER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE: ; OTHER INFORMATION: SCFV EPCAMXCD3 with MIO mutant in anti-CD3 part US-10-682-845-69
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                                                                                                                                                                                              ; OTHER INFORMATION: scFv EpCAMxCD3 with M13 mutant in anti-CD3 US-10-682-845-73
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                                                                                                                      Best Loc
Matches
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Best Local Similarity
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                TYPE: PRT ORGANISM: artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                      LENGTH: 492
                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQLTQSQKFMSTSVGDRVSVTCKASQ-----NVGTNVAWYQQKPGQSPKALIYSASYR
                                                                               1 ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR 60
ESGYPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WSG-GSTDYNAAFISRLSISKDNSKSQVFFKMNSLQANDTAIYYCARMENWS--FAYWGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGSGGGGSQVK-LQESGPGLVQPSQSLSITCTVSGPSLTSYGVHWVRQSPGKGLEWLGVI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGSGGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDI 180
                                               DIQLTQSQKFMSTSVGDRVSVTCKASQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGYINPSRGYTNYNOKFKDKATLTTDKSSSTAYMOLSSLTSEDSAVYYCARYYDDHYCLD 360
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                                                                                                                       44;
                                                                                                                      Score 1401; DB 4;
Pred. No. 1.6e-85;
4; Mismatches 55;
                                               -NVGTNVAWYQQKPGQSPKALIYSASYR
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	301 IGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLD 360 	B 8
	241 GTTVTVSSGGGGSDIKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEW 300 	음 성
	181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQ 240	B 8
	121 GGSGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDI 180 	음 경
~	61 ESGYPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG 120 	용 성
	1 ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR 60 	ል ያ
	Query Match 68.5%; Score 1401; DB 4; Length 492; Best Local Similarity 70.7%; Pred. No. 1.6e-85; Matches 263; Conservative 44; Mismatches 55; Indels 10; Gaps 4;	3 8 0
	ORGANISM: artificial sequence FEATURE: OTHER INFORMATION: scFv EpCAMxCD3 with M69 mutant in anti-CD3 part -10-682-845-85	Ś
	SEQ ID NO 85 LENGTH: 492 TYPE: PRT	 ن
- T	OR FILING DATE: 2002-10-11 IBER OF SEQ ID NOS: 89 TWARE: Patentin version 3.1	
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	CURRENT FILING DATE: 2003-10-10	
	APPLICANT LARGASCHIA, Antonio APPLICANT LARGASCHIA, Antonio TITLE OF INVENTION: Potent T cell modulating molecules	
	RESULT 15 US-10-682-845-85 ; Sequence 85, Application US/10682845 ; Septient No. US20040162411A1 . GENERAL TRECRMATION.	RES US-
	351 YWGQGTTLTVSS 362	문
	361 YWGQGTTLTVSS 372	ફ
	291 IGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYNDQYCLD 350	밁
	301 IGYINPSRGYTNYNQKFKDKATLITDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLD 360	ş
	231 GTTVTVSSGGGGSDIKLQQSGAELARPGASVKMSCKTSGYTFTRYTWHWVKQRPGQGLEW 290	뮹
	241 GTTVTVSSGGGGSDIKLQQSGAELARPGASVKMSCKTSGYTFTRYTWHWVKQRPGQGLEW 300	ફ
	181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQ 240 : : : ::: : ::: : :	8 8
_		Db
	121 GGSGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDI 180	8

Search completed: March 6, 2006, 13:21:48 Job time : 81 secs

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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

24	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ	ហ	4	ω	N	۲	No.	Result
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Anti-CD	Adv21529 Mature to	Anti-CD		Deimmun	ω	Anti-CD	ω	Adz83625 CD3 speci	_		CD3	CD3	CD3	_	Adz83629 CD3 speci	-	CB	_	spec	Adv66116 Anti-CD3-	Ant		Description	

4.5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25
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Adz83562	Adzesses	AQ283564	AGZUJSEU	Adz83556	Adzesse	Adz83570	Adz83568	Adz835/2	Aae22193	Adz83439	AGZ83433	Adz835/6	Adz83578	A02835/4	ACVIASSU	Advzisis	Aay43/49	Aea5244/	ACVIASSE	AGZ83582
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ALIGNMENTS

RESULT 1 AEA36900 chimeric antibody; cytostatic; antimicrobial; antiallergic; antinflammatory; virucide; antiparasitic; immunomodulatory; immunosuppressive; vaccine; bispecific antibody; cancer; inflammation; immune disorder; infection; viral infection; allergy; parasitic infection; graft versus host disease. Synthetic. 25-AUG-2005 (first entry) AEA36900; AEA36900 standard; protein; 378 AA. 22-DEC-2003; 2003US-00743697. 23-JUN-2005. US2005136050-A1 Anti-CD3xanti-EpCAM bispecific chimeric antibody Kufer P, 22-DEC-2003; 2003US-00743697. (KUFE/) KUFER P. (BERR/) BERRY M. (BAEU/) BAEUERLE P. ITIN C. Berry M, Baeuerle ָש Itin ü

New bispecific antibody comprising two antibody variable domains on a single polypeptide chain, useful in preparing a composition for treating or preventing proliferative, immunological, infectious or graft-versushost disease.

WPI; 2005-444079/45.

Claim 24; SEQ ID NO 1; 12pp; English.

The invention relates to a bispecific antibody comprising two antibody variable domains on a single polypeptide chain, where a first portion of the bispecific antibody is capable of recruiting the activity of a human immune effector cell by specifically binding to an effector antigen located on the human immune effector cell, the first portion consisting

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of one antibody variable domain; and a second portion of the bispecific antibody is capable of specifically binding to a target antigen other than the effector antigen, the target antigen being located on a target cell other than the human immune effector cell, and the second portion comprising an antibody variable domain. The bispecific antibody is useful in preparing a composition for treating, preventing or ameliorating a proliferative disease, a tumorous disease, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, an viral disease, an allergic reaction, a parasitic reaction, a graft-versus host disease or a host-versus-graft disease. This sequence corresponds to the chimeric anti-CD3xanti-EpCAM bispecific antibody of the invention.
                                             31-MAY-2003; 2003EP-00012133.
31-MAY-2003; 2003EP-00012134.
                                                                                                                                                                                                                bispecific single chain antibody; epithelial cell adhesion molecule;
EpCAM; CD3; tumor; cancer; cytostatic.
                                                                                                                           09-DEC-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 378 AA;
                                                                                         26-MAY-2004; 2004WO-EP005687
                                                                                                                                                       WO2004106383-A1
                                                                                                                                                                                                                                                          Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID
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                  (MICR-) MICROMET AG
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Pred. No. 1.
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ARSSULT 3
ADV66116
ID ADV6
XX ADV6
AC ADV6
XX ADV6
XX ADV6
XX ADV6
XX BAT1
XX

24-FEB-2005

(first entry)

ADV66116 standard; protein;

521

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bispecific single chain antibody; epithelial EpCAM; CD3; tumor; cancer; cytostatic.

cell

molecule;

SEQ ID

Unidentified. WO2004106383-A1 Anti-CD3-anti-EpCAM bispecific single chain antibody -

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New pharmaceutical composition having a bispecific single chain antibody construct, useful for preventing, treating or ameliorating a tumorous disease, such as an epithelial or minimal residual cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 521 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kufer P, Berry M, Offner S, Br. Kohleisen B, Lenkkeri-Schuetz U,
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                                                                                                                                                                                                                                                                     GGSGGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDI
                                                                                                                                                                                                                                                                                                                                  ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG
                        YWGQGTTLTVSS
                                                                                                                                         GTTVTVSSGGGGSDIKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEW
                                                                                                                                                                                                       FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVXFCARLRNWDEPMDYWGQ
YWGQGTTLTVSS
                                                                               IGYINPSRGYTNYNQKFKDKATLITDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLD
                                                                                                                         GTTVTVSSGGGGSDIKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEW
                                                                                                                                                                                    FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQ
                                                                                                                                                                                                                                                 GGSGGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDI
                                                                                                                                                                                                                                                                                                               ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG
                                                                                                                                                                                                                                                                                                                                                                           ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR
                                                            IGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                97.7%; 5-
100.0%; Pr
391
                             372
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1998; DB 9;
Pred. No. 1.5e-116;
0; Mismatches 0;
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RESULT 4
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAY-2003; 2003EP-00012133.
31-MAY-2003; 2003EP-00012134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New pharmaceutical composition having a bispecific single chain antibody construct, useful for preventing, treating or ameliorating a tumorous disease, such as an epithelial or minimal residual cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2004; 2004WO-EP005687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 521
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           14-JUL-2005
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                                                                                                                                                                                                                                                                                                                                                          ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG
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                                                                                                                                                                                                                   GTTVTVSSGGGGSDIKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEW
                                                                                                                                                                                                                                                     FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQ
                                                                                                                                                                                                                                                                                                  GGSGGGGSEVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWVGDI
                                                                                                                                                                                                                                                                                                                                              ESGVPDRFTGSGSGTDFTLTTSSVQAEDLAVYYCQNDYSYPYTFGGGTKLEIKGGGGSGG
                                                                                                                                                                           standard;
                                                                                                                                    YWGOGTTLTVSS
                                                                                                                                                          SEQ ID NO 39; 227pp; English
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Lenkkeri-Schuetz
              (first
                                                         protein;
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Pred. No. 1.2e-112;
3; Mismatches 8;
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U, Baeuerle
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Best Local S
Matches 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cytotoxically active CD3 specific binding construct comprises domain specifically binding to human CD3 and an Ig-derived second domain, useful for treating, preventing, or ameliorating, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2003; 2003EP-00023581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                     121
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                                                                                                                                                                                                                                                                      ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                              ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG
                                                                                                                                                                                                                                        496
                 GTTVTVSSGGGGSDIKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEW
                                                                             FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQ
                                                                                                                                                                              ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG
FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQ
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Williams S;
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Pred. No. 2.4e-112;
2; Mismatches 6;
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Query Match
Best Local S
Matches 354
                                                                                                                                                                  proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, allergic reactions, parasitic reactions, graft-versus-bost diseases, or host-versus-graft diseases. The cytotoxically active CD3 specific binding construct is useful for treating, preventing, or ameliorating proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, allergic reactions, parasitic reactions, graft-versus-bost diseases, or host-versus-graft diseases. The present sequence represents the amino acid sequence of a CD3 specific binding construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain. The CD3 specific binding construct above or the construct produced by the process, nucleic acid molecule, vector, or host is useful for the preparation of a pharmaceutical composition for the prevention, treatment, or amelioration of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cytotoxically active CD3 specific binding construct comprises domain specifically binding to human CD3 and an Ig-derived second domain, useful for treating, preventing, or ameliorating, e.g.
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mes 354; Conserv
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Williams S;
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2; Mismatches
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Matches 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 496
                                                                                                                                                           Synthetic.
                                                                                                                                                                                    neoplasm; inflammation; immune disorder; infection; allergy; graft versus host disease; Cytostatic; Antiinflammatory; Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.
                                                                                                                                                                                                                                                                     14-JUL-2005
                                                                                                                                                                                                                                                                                                                       ADZ83615 standard; protein; 496
                                                                                                                                                                                   Immunosuppressive;
  Hofmeister
                                                                                                                                    WO2005040220-A1
                                                                               15-OCT-2004; 2004WO-EP011646
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  Kohleisen
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Pred. No. 2.4e-112;
L2; Mismatches 6;
  Lenkkeri-Schuetz U,
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RESULT 8
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ID ADZ8
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AC ADZ8
XX
DT 14-J
XX
DE CD3

ADZ83629

standard;

protein;

14-JUL-2005

(first entry)

CD3 specific binding construct

SEQ ID NO

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The invention relates to a cytotoxically active CD3 specific binding CC construct comprises a first domain specifically binding to human CD3 and CC an Ig-derived second binding domain. The CD3 specific binding construct CC above or the construct produced by the process, nucleic acid molecule, CC vector, or host is useful for the preparation of a pharmaceutical CC composition for the prevention, treatment, or amelioration of a CC proliferative disease, a tumor, an inflammatory disease, viral disease, CC disorder, an autoimmune disease, an infectious disease, viral disease, or CC host-versus-graft diseases. The cytotoxically active CD3 specific binding CC construct is useful for treating, preventing, or ameliorating CC proliferative disease, a tumor, an inflammatory disease, an immunological CC disorder, an autoimmune disease, an infectious disease, an immunological CC proliferative disease, a tumor, an inflammatory disease, an immunological CC disorder, an autoimmune disease, an infectious disease, viral disease, or host-versus-graft diseases. The present sequence represents the amino CC acid sequence of a CD3 specific binding construct.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carr FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 237; 639pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 496 AA;
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                  YWGQGTTLTVSS 372
                                                                        IGYINPSRGYTNYADSVKGRFTITTDKSTSTAYMELSSLRSEDTATYYCARYYDDHYCLD
                                                                                                     | IGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1892; DB 9;
Pred. No. 5.6e-110;
.2; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 496;
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300

240 240

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The invention relates to a cytotoxically active CD3 specific binding CC construct comprises a first domain specifically binding to human CD3 and CC an Ig-derived second binding domain. The CD3 specific binding construct CC above or the construct produced by the process, nucleic acid molecule, corrector, or host is useful for the preparation of a pharmaceutical CC composition for the prevention, treatment, or amelioration of a pharmaceutical CC composition for the prevention, treatment, or amelioration of a proliferative disease, a tumor, an inflammatory disease, viral disease, allergic reactions, parasitic reactions, graft-versus-host disease, or CC host-versus-graft diseases. The cytotoxically active CD3 specific binding CC construct is useful for treating, preventing, or ameliorating CC construct is useful for treating, preventing, or ameliorating CC disorder, an autoimmune disease, an inflammatory disease, an immunological CC disorder, an autoimmune disease, an inflammatory disease, viral disease, CC callergic reactions, parasitic reactions, graft-versus-host diseases, or CC host-versus-graft diseases. The present sequence represents the amino CC acid sequence of a CD3 specific binding construct.
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GTTVTVSSGGGGSDVQLVQSGAEVKKPGASVKVSCKASGYTFTRYTMHWVRQAPGQGLEW
                                        GTTVTVSSGGGGSDIKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEW
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Williams
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Pred. No. 5.6e-110;
L2; Mismatches 12;
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ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR

Query Match Best Local : Matches

Similarity

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                            The invention relates to a cytotoxically active CD3 specific binding CC construct comprises a first domain specifically binding to human CD3 and CC an Ig-derived second binding domain. The CD3 specific binding construct CC above or the construct produced by the process, nucleic acid molecule, composition for the prevention, treatment, or amelioration of a manunological CC composition for the prevention, treatment, or amelioration of a pharmaceutical CC composition for the prevention, treatment, or amelioration of a pharmaceutical CC disorder, an autoimmune disease, an inflammatory disease, viral disease, or CC allergic reactions, parasitic reactions, graft-versus-host diseases, or CC construct is useful for treating, preventing, or ameliorating CC construct is useful for treating, preventing, or ameliorating CC proliferative disease, a tumor, an inflammatory disease, an immunological CC disorder, an autoimmune disease, an infectious disease, viral disease, or CC disease; an autoimmune disease, an infectious disease, viral disease, or CC construct of the parasitic reactions, graft-versus-host diseases, or CC construct of diseases. The present sequence represents the amino CC caid sequence of deimmunized construct 5-10xanti-CD3.
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Immunosuppressive; Virucide;
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 Sequence
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The invention relates to a cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain. The CD3 specific binding construct above or the construct produced by the process, nucleic acid molecule, vector, or host is useful for the preparation of a pharmaceutical composition for the prevention, treatment, or amelioration of a proliferative disease, a tumor, an inflammatory disease, an immunological
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Carr FJ, Hamilton
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                             GLEWIGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDH
                                                                                                         EGTSTGSGGSGGADDVQLVQSGAEVKKPGASVKVSCKASGYTFTRYTMHWVRQAPGQ
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GLEWIGYINPSRGYTNYNQKFKDRVTITTDKSTSTAYMELSSLRSEDTAVYYCARYYDDH
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Pred. No. 6.4e-108;
                                                                                                                                         Lenkkeri-Schuetz
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ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYMASTR
ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGG

120

Query Match Best Local 9 Matches 359

Local Similarity

90.9%;

; Score 1859; DB 9; ; Pred. No. 6.4e-108; 11; Mismatches 6;

Length 496; Indels 12

124;

Gaps

Conservative

ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTR

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                                      CC The invention relates to a cytotoxically active CD3 specific binding CC construct comprises a first domain specifically binding to human CD3 and CC an ig-derived second binding domain. The CD3 specific binding construct CC above or the construct produced by the process, nucleic acid molecule, CC vector, or host is useful for the preparation of a pharmaceutical CC composition for the prevention, treatment, or amelioration of a CC proliferative disease, a tumor, an inflammatory disease, viral disease, or CC disorder, an autoimmune disease, an infectious disease, viral diseases, or CC host-versus-graft diseases. The cytotoxically active CD3 specific binding CC construct is useful for treating, preventing, or ameliorating CC construct disease, a tumor, an inflammatory disease, an immunological CC construct an autoimmune disease, a nimentory disease, an immunological CC disorder, an autoimmune disease, an infectious disease, viral disease, or allergic reactions, parasitic reactions, graft-versus-host diseases, or cC disorder, an autoimmune disease, an infectious disease, or allergic reactions, parasitic reactions, graft-versus-host diseases, or cC chost-versus-graft diseases. The present sequence represents the amino CC acid sequence of a CD3 specific binding construct.
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Sequence
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                                                           New cytotoxically active CD3 specific binding construct comprises domain specifically binding to human CD3 and an Ig-derived second domain, useful for treating, preventing, or ameliorating, e.g.
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Carr FJ, Ham
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                                                                                                                                                                                                                                                                                                                                                                                                 ADZ83436 standard; protein;
 The invention relates to a cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3
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                              58; 639pp; English.
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                                                                                                                                   n B, Lenkkeri-Schuetz U, Williams S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC an Ig-derived second binding domain. The CD3 specific binding construct CC above or the construct produced by the process, nucleic acid molecule, CC vector, or host is useful for the preparation of a pharmaceutical CC composition for the prevention, treatment, or amelioration of a CC proliferative disease, a tumor, an inflammatory disease, an immunological CC disorder, an autoimmune disease, an infectious disease, viral disease, or CC allergic reactions, parasitic reactions, graft-versus-host diseases, or CC construct is useful for treating, preventing, or ameliorating CC construct is useful for treating, preventing, or ameliorating CC proliferative disease, a tumor, an inflammatory disease, an immunological CC disorder, an autoimmune disease, an infectious disease, viral disease, CC allergic reactions, parasitic reactions, graft-versus-host disease, or CC host-versus-graft diseases. The present sequence represents the amino CC acid sequence of deimmunized construct 4-lxanti-CD3.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.6
Matches 337; Conservative
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                YWGQGTTLTVSS
                                                                             IGYINDSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLD
                                                                                                                                                 GTTVTVSSGGGGSDIKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEW
                                                                                                                                                                                                           FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEFMDYWGQ
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                                                             GTTVTVSSGGGGSDVQLVQSGAEVKKPGASVKVSCKASG
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; Pred. No. 4.9e-106;
15; Mismatches 20;
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neoplasm; inflammation; immune disorder; infection; allergy; graft versus host disease; Cytostatic; Antiinflammatory; Immunosuppressive; Virucide; Antibacterial; Antiallergic; An 16-OCT-2003; 2003EP-00023581 Synthetic CD3 specific binding 14-JUL-2005 ADZ83619 15-OCT-2004; 2004WO-EP011646. WO2005040220-A1 standard; (first entry) protein; construct 496 SEQ ä ŏ 241.

Antiallergic; Antiparasitic.

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The invention relates to a cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and CC an Ig-derived second binding domain. The CD3 specific binding construct by the construct produced by the process, nucleic acid molecule, vector, or host is useful for the preparation of a pharmaceutical composition for the prevention, treatment, or amelioration of a composition for the prevention, treatment, or amelioration of a pharmaceutical composition for the prevention, treatment, or amelioration of a composition for the prevention, an inflammatory disease, an immunological composition for treatment in the crious disease, viral disease, or compositions, parasitic reactions, graft-versus-host disease, or construct is useful for treating, preventing, or ameliorating construct is useful for treating, preventing, or ameliorating construct is useful for treating, preventing, or ameliorating construct an autoimmune disease, an inflammatory disease, an immunological disease, an autoimmune disease, an inflammatory disease, viral disease, allergic reactions, parasitic reactions, graft-versus-host diseases, or host-versus-graft diseases. The present sequence represents the amino call disease of a cld sequence of a CD3 specific binding construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 349;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferative disease.
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YCLDYWGQGTTLTVSS
                                                                                                                                                    GLEWIGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDH 356
                                                                                           GLEWIGYINPSRGYTNYADSVKGRFTITTDKSTSTAYMELSSLRSEDTATYYCARYYDDH
                                                                                                                                                                                                                                                                                                                                    YDTSKVASGVPARFSGSGSGTDYSLTINSLEAEDAATYYCQQWSSNPLTFGGGTKVEIKG
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                                                                                                                                                                                                               EGTSTGSGGSGGSGGADDVQLVQSGAEVKKPGASVKVSCKASGYTFTRYTMHWVRQAPGQ
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ton AA, Williams
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70.4%;
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Pred. No. 1.5e-105;
L1; Mismatches 12;
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                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain, useful for treating, preventing, or ameliorating, e.g. proliferative disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 247; 639pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hofmeister R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2003; 2003EP-00023581
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                                                                                                                                                    Local Similarity
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lton AA, Williams S;
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Pred. No. 1.5e
11; Mismatches
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1.5e-105;
hes 12;
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